<110> CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE

<120> EXPRESSION SYSTEMS OF TOXIC PROTEINS, VECTORS AND PROCESS FOR MANUFACTURING TOXIC PROTEINS

<130> B14143 EE <140> <141> <150> FR N □ 02 11676 <151> 2002-09-20 <160> 53 <170> PatentIn Ver. 2.1 <210>1 <211>37 <212> PRT <213> Hepatitis C virus Met Ile Ala Gly Ala His Trp Gly Val Leu Ala Gly Ile Ala Tyr Phe 10 Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Val Leu Leu Leu Phe 25 30 Ala Gly Val Asp Ala 35 <210>2 <211>31 <212> PRT <213> Hepatitis C virus <400> 2 Met Glu Tyr Val Val Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Val 5 10 Cys Ser Cys Leu Trp Met Met Leu Leu Ile Ser Gln Ala Glu Ala 20 25 30 <210>3 <211>111 <212> DNA <213> Hepatitis C virus <400> 3 atgategetg gtgeteaetg gggtgttetg getggtateg ettaettete tatggttggt 60 aactgggeta aagttetggt tgttetgetg etgttegetg gtgttgaege t

<210> 4 <211> 93 <212> DNA

<213> Hepatitis C virus

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tggatgatg
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<210> 5 <211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: oligonucleotide (+) of insertion into pT7-7

<400> 5

gggaatgcca tatgatcgct ggtg

24

<210>6

<211>23

<212> DNA

<213> Artificial sequence

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<223> Description of the artificial sequence: oligonucleotide (-) of insertion into pT7-7

<400> 6

gcatatcgat ctaagcgtca aca

23

<210>7

<211> 131

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: TME1 coding sens DNA + 3' cla I site

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<210>8

<211> 131

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: anticodant sens DNA + 5' cla I site

<400> 8

gcatatcgat ctaagcgtca acaccagcga acagcagcag aacaaccaga actttagccc 60 agttaccaac catagagaag taagcgatac cagccagaac accccagtga gcaccagcga 120 tcatatggca t

<210> 9

<211> 74

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<212> DNA
<213> Artificial sequence
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<223> Description of the artificial sequence:
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   TME1
<400>9
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ggttggtaac tggg
<210> 10
<211>79
<212> DNA
<213> Artificial sequence
<223> Description of the artificial sequence:
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<400> 10
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agttaccaac catagagaa
<210> 11
<211>22
<212> DNA
<213> Artificial sequence
<220>
<223> Description of the artificial sequence:
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    the dp site
<400> 11
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ggatccatgg aatacgttgt tc
<210>12
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 <212> DNA
 <213> Artificial sequence
 <220>
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    the dp site
 <400> 12
                                                   28
 ggatccgacc cgatggaata cgttgttc
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 <223> Description of the artificial sequence:
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<210> 15 <211> 26 <212> DNA <213> Artificial sequence	
<220> <223> Description of the artificial sequence: oligonucleotide (+) of insertion into pT7-7	
<400> 15 cgcatatgga cccgatcgct ggtgct	26
<210> 16 <211> 24 <212> DNA <213> Artificial sequence <220>	
<223> Description of the artificial sequence: oligonucleotide (-) of insertion into pT7-7	
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<210> 17 <211> 19 <212> DNA <213> Artificial sequence	
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<212> DNA

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<400> 17

<210> 18 <211>28

<213> Artificial sequence

19

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<210> 19
<211> 103
<212> DNA
<213> Artificial sequence
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<223> Description of the artificial sequence: sens DNA
   coding TME2 + 5' Nde I site and 3□Hind III site
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ctgtggatga tgctgctgat ctctcaggct gaagcttaag ctt
<210> 20
<211> 103
<212> DNA
<213> Artificial sequence
<220>
<223> Description of the artificial sequence: sens DNA
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<400> 20
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cgtcagccag cagcaggaac agcagaacaa cgtattccat atg
<210>21
<211>68
<212> DNA
<213> Artificial sequence
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<223> Description of the artificial sequence:
    sens oligonucleotide (+) coding for the synthesis
    of TME2
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 ctgtggat
 <210> 22
 <211>57
 <212> DNA
 <213> Artificial sequence
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 <223> Description of the artificial sequence:
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    of TME2
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<211>19
<212> DNA
<213> Artificial sequence
<220>
<223> Description of the artificial sequence:
   oligonucleotide (+) of insertion into pGEXKT without
   the dp site
<400> 23
                                              19
ggatccgaat acgttgttc
<210> 24
<211>25
<212> DNA
<213> Artificial sequence
<220>
<223> Description of the artificial sequence:
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   the dp site
<400> 24
                                                 25
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<210> 25
<211>30
<212> DNA
<213> Artificial sequence
<220>
<223> Description of the artificial sequence:
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    the dp site
 <400> 25
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<210> 26
 <211> 27
 <212> DNA
 <213> Artificial sequence
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 <223> Description of the artificial sequence:
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 <400> 26
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 <210> 27
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 <212> DNA
 <213> Artificial sequence
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<210>23

<223> Description of the artificial se oligonucleotide (-) of insertion into p17-7

<400> 27

cagaatteet aagetteage etgagag

27

<210>28

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: end of the GST followed by the thrombine site

<400>28

Ser Asp Leu Ser Gly Gly Gly Gly Leu Val Pro Arg Gly Ser

5 10 15

<210>29

<211>717

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: DNA coding for GST protein in the pGEXKT vector

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<210> 30

<211> 327

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: DNA coding for the thioredoxine in the pET32a+ vector

<400> 30

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<210> 31 <211> 4969 <212> DNA <213> Artificial sequence

<220>

223> Description of the artificial sequence: plasmide expressing pGEXKT

<400> 31

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<213> Artificial sequence

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<223> Description of the artificial sequence: plasmide expressing pET32a+

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<223> Description of the artificial sequence: expression system coding for fusion protein GST-DP-TME1

<400> 34

atgtccccta tactaggtta ttggaaaatt aagggccttg tgcaacccac tcgacttctt 60 ttggaatatc ttgaagaaaa atatgaagag catttgtatg agcgcgatga aggtgataaa 120 tggcgaaaca aaaagtttga attgggtttg gagtttccca atcttcctta ttatattgat 180 ggtgatgtta aattaacaca gtctatggcc atcatacgtt atatagctga caagcacaac 240 atgttgggtg gttgtccaaa agagcgtgca gagatttcaa tgcttgaagg agcggttttg 300 gatattagat acggtgtttc gagaattgca tatagtaaag actttgaaac tctcaaagtt 360 gattttctta gcaagctacc tgaaatgctg aaaatgttcg aagatcgttt atgtcataaa 420 acatatttaa atggtgatca tgtaacccat cctgacttca tgttgtatga cgctcttgat 480 gttgttttat acatggaccc aatgtgcctg gatgcgttcc caaaattagt ttgttttaaa 540 aaacgtattg aagctatccc acaaattgat aagtacttga aatccagcaa gtatatagca 600

tggcctttgc agggctggca agccacgttt ggtg accatcctcc aaaatcggat 660 ctgtctggtg gtggtggtgg tctggttccg cgtggateg acccgatcgc tggtgctcac 720 tggggtgttc tggctggtat cgcttacttc tctatggttg gtaactgggc taaagttctg 780 gttgttctgc tgctgttcgc tggtgttgac gct 813

<210> 35

<211> 513

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression system coding for fusion protein TrX-DP-TME1

<400> 35

atgagegata aaattattea eetgactgae gacagttttg acaeggatgt acteaaageg 60 gacggggega teetegtega tttetgggea gagtggtgeg gteegtgeaa aatgategee 120 eegattetgg atgaaatege tgacgaatat eagggeaaac tgacegttge aaaaetgaac 180 ategateaaa accetggeae tgegeegaaa tatggeatee gtggtateee gactetgetg 240 etgtteaaaa acggtgaagt ggeggeaace aaagtgggtg eaetgetaa aggteagttg 300 aaagagttee tegacgetaa eetggeeggt tetggttetg gateteeaaa ateggatetg 360 tetggtggtg gtggtggtet ggtteegegt ggateegaee egategetgg tgeteaetgg 420 ggtgttetgg etggtatege ttaettetet atggttggta aetgggetaa agttetggtt 480 gttetgetge tgttegetgg tgttgaeget tag

<210> 36

<211>117

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression system coding for fusion protein M-DP-TME1

<400> 36

atggaccega tegetggtge teaetgggt gttetggetg gtategetta ettetetatg 60 gttggtaact gggetaaagt tetggttgtt etgetgetgt tegetggtgt tgacget 117

<210> 37

<211> 795

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression system coding for fusion protein GST-DP-TME2

<400> 37

atgtccccta tactaggtta ttggaaaatt aagggccttg tgcaacccac tcgacttctt 60 ttggaatatc ttgaagaaaa atatgaagag catttgtatg agcgcgatga aggtgataaa 120 tggcgaaaca aaaagtttga attgggtttg gagtttccca atcttcctta ttatattgat 180 ggtgatgtta aattaacaca gtctatggcc atcatacgtt atatagctga caagcacaac 240 atgttgggtg gttgtccaaa agagcgtgca gagatttcaa tgcttgaagg agcggttttg 300 gatattagat acggtgttc gagaattgca tatagtaaag actttgaaac tctcaaagtt 360 gattttcta gcaagctacc tgaaatgctg aaaatgttcg aagatcgttt atgtcataaa 420 acatatttaa atggtgatca tgtaacccat cctgacttca tgttgtatga cgctcttgat 480 gttgtttat acatggaccc aatgtgcctg gatgcgtcc caaaattagt ttgttttaaa 540 aaacgtattg aagctatccc acaaattgat aagtacttga aatccagcaa gtatatagca 600 tggcctttgc agggctggca agccacgttt ggtggtggcg accatcctcc aaaatcggat 660

ctgtctggtg gtggtggtgg tctggttccg cgtg acccggaata cgttgttctg 720 ctgttcctgc tgctggctga cgctcgtgtt tgctcttgc tgtggatgat gctgctgatc 780 tctcaggctg aagct 795

<210>38

<211>486

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression system coding for fusion protein TrX-DP-TME2

<400> 38

atgagegata aaattattea eetgactgae gacagttttg acaeggatgt acteaaageg 60 gacggggega teetegtega tttetgggea gagtggtgeg gteegtgeaa aatgategee 120 eegattetgg atgaaatege tgacgaatat eagggeaaac tgacegttge aaaaetgaae 180 ategateaaa accetggeae tgegeegaaa tatggeatee gtggtateee gactetgetg 240 etgtteaaaa acggtgaagt ggeggeaaee aaagtgggtg eactgtetaa aggteagttg 300 aaagagttee tegacgetaa eetggeeggt tetggttetg gatetgatet gtetggtggt 360 ggtggtggte tggtteegeg tggateegae eeggaataeg ttgttetget gtteetgetg 420 etggetgaeg etegtgtttg etettgeetg tggatgatge tgetgatete teaggetgaa 480 gettag 486

<210>39

<211>99

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression system coding for fusion protein M-DP-TME2

<400>39

atggacccgg aatacgttgt tctgctgttc ctgctgctgg ctgacgctcg tgtttgctct 60 tgcctgtgga tgatgctgct gatctctcag gctgaagct 99

<210>40

<211> 5082

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression vector pGEXKT-dp-Pt(TME1)

<400> 40

acgttatega etgeaeggtg caceaatget tetggegtea ggeagceate ggaagetgtg 60 gtatggetgt geaggtegta aateaetgea taattegtgt egeteaagge geaeteeegt 120 tetggataat gttttttgeg eegacateat aaeggttetg geaaatatte tgaaatgage 180 tgttgacaat taateategg etegtataat gtgtggaatt gtgageggat aaeaatttea 240 cacaggaaac agtatteatg teecetatae taggttattg gaaaattaag ggeettgtge 300 aaeceaeteg aettettttg gaatatettg aagaaaaata tgaagageat ttgtatgage 360 gegatgaagg tgataaatgg egaaacaaaa agtttgaatt gggtttggag ttteecaate 420 tteettatta tattgatggt gatgttaaat taaeacagte tatggeeate ataegttata 480 tagetgacaa geacaacatg ttgggtggtt gteeaaaaga gegtgeagag attteaatge 540 ttgaaggage ggttttggat attagataeg gtgtttegag aattgeatat agtaaagaet 600 ttgaaactet caaagttgat tttettagea agetaeetga aatgetgaaa atgttegaag 660 ategttatg teataaaaca tatttaaatg gtgateatgt aaeceateet gaetteatgt 720

tgtatgacgc tcttgatgtt gttttataca tggacç gcctggat gcgttcccaa 780 aattagtttg ttttaaaaaa cgtattgaag ctatcccaea aattgataag tacttgaaat 840 ccagcaagta tatagcatgg cctttgcagg gctggcaagc cacgtttggt ggtggcgacc 900 atcctccaaa atcggatctg tctggtggtg gtggtggtct ggttccgcgt ggatccgacc 960 cgatcgctgg tgctcactgg ggtgttctgg ctggtatcgc ttacttctct atggttggta 1020 actgggctaa agttctggtt gttctgctgc tgttcgctgg tgttgacgct taggaattca 1080 tcgtgactga ctgacgatct gcctcgcgcg tttcggtgat gacggtgaaa acctctgaca 1140 catgcagctc ccggagacgg tcacagcttg tctgtaagcg gatgccggga gcagacaagc 1200 ccgtcagggc gcgtcagcgg gtgttggcgg gtgtcggggc gcagccatga cccagtcacg 1260 tagcgatagc ggagtgtata attettgaag acgaaagggc etcgtgatac gcetattttt 1320 ataggttaat gtcatgataa taatggtttc ttagacgtca ggtggcactt ttcggggaaa 1380 tgtgcgcgga acccctattt gtttattttt ctaaatacat tcaaatatgt atccgctcat 1440 gagacaataa ccctgataaa tgcttcaata atattgaaaa aggaagagta tgagtattca 1500 acatttccgt gtcgccctta ttcccttttt tgcggcattt tgccttcctg tttttgctca 1560 cccagaaacg ctggtgaaag taaaagatgc tgaagatcag ttgggtgcac gagtgggtta 1620 categaactg gateteaaca geggtaagat cettgagagt tttegeeeg aagaaegttt 1680 tccaatgatg agcactttta aagttctgct atgtggcgcg gtattatccc gtgttgacgc 1740 cgggcaagag caactcggtc gccgcataca ctattctcag aatgacttgg ttgagtactc 1800 accagtcaca gaaaagcatc ttacggatgg catgacagta agagaattat gcagtgctgc 1860 cataaccatg agtgataaca ctgcggccaa cttacttctg acaacgatcg gaggaccgaa 1920 ggagctaacc gcttttttgc acaacatggg ggatcatgta actcgccttg atcgttggga 1980 accggagetg aatgaageca taccaaacga egagegtgae accaegatge etgeageaat 2040 ggcaacaacg ttgcgcaaac tattaactgg cgaactactt actctagctt cccggcaaca 2100 attaatagac tggatggagg cggataaagt tgcaggacca cttctgcgct cggcccttcc 2160 ggctggctgg tttattgctg ataaatctgg agccggtgag cgtgggtctc gcggtatcat 2220 tgcagcactg gggccagatg gtaagccctc ccgtatcgta gttatctaca cgacggggag 2280 tcaggcaact atggatgaac gaaatagaca gatcgctgag ataggtgcct cactgattaa 2340 gcattggtaa ctgtcagacc aagtttactc atatatactt tagattgatt taaaacttca 2400 tttttaattt aaaaggatet aggtgaagat eetttttgat aateteatga eeaaaateee 2460 ttaacgtgag ttttcgttcc actgagcgtc agaccccgta gaaaagatca aaggatcttc 2520 ttgagateet ttttttetge gegtaatetg etgettgeaa acaaaaaaac eacegetace 2580 ageggtggtt tgtttgeegg ateaagaget aceaactett ttteegaagg taaetggett 2640 cagcagageg cagataceaa atactgteet tetagtgtag cegtagttag gecaccaett 2700 caagaactet gtageacege etacatacet egetetgeta ateetgttae eagtggetge 2760 tgccagtggc gataagtcgt gtcttaccgg gttggactca agacgatagt taccggataa 2820 ggcgcagcgg tcgggctgaa cggggggttc gtgcacacag cccagcttgg agcgaacgac 2880 ctacaccgaa ctgagatacc tacagcgtga gctatgagaa agcgccacgc ttcccgaagg 2940 gagaaaggeg gacaggtate eggtaagegg cagggtegga acaggagage geacgaggga 3000 getteeaggg ggaaaegeet ggtatettta tagteetgte gggtttegee acetetgaet 3060 tgagegtega tttttgtgat getegteagg ggggeggage etatggaaaa aegeeageaa 3120 egeggeettt ttaeggttee tggeettttg etggeetttt geteaeatgt tettteetge 3180 gttatcccct gattctgtgg ataaccgtat taccgccttt gagtgagctg ataccgctcg 3240 ccgcagccga acgaccgagc gcagcgagtc agtgagcgag gaagcggaag agcgcctgat 3300 geggtatttt eteettaege atetgtgegg tattteaeae egeataaatt eegaeaeeat 3360 cgaatggtgc aaaacctttc gcggtatggc atgatagcgc ccggaagaga gtcaattcag 3420 ggtggtgaat gtgaaaccag taacgttata cgatgtcgca gagtatgccg gtgtctctta 3480 tcagaccgtt tcccgcgtgg tgaaccaggc cagccacgtt tctgcgaaaa cgcgggaaaa 3540 agtggaagcg gcgatggcgg agctgaatta cattcccaac cgcgtggcac aacaactggc 3600 gggcaaacag tegttgetga ttggegttge cacetecagt etggecetge acgegeegte 3660 gcaaattgtc gcggcgatta aatctcgcgc cgatcaactg ggtgccagcg tggtggtgtc 3720 gatggtagaa cgaagcggcg tcgaagcctg taaagcggcg gtgcacaatc ttctcgcgca 3780 acgcgtcagt gggctgatca ttaactatcc gctggatgac caggatgcca ttgctgtgga 3840 agetgeetge actaatgtte eggegttatt tettgatgte tetgaceaga cacceateaa 3900 cagtattatt ttctcccatg aagacggtac gcgactgggc gtggagcatc tggtcgcatt 3960 gggtcaccag caaatcgcgc tgttagcggg cccattaagt tctgtctcgg cgcgtctgcg 4020 tetggetgge tggeataaat ateteaeteg caatcaaatt cageegatag eggaaeggga 4080 aggegactgg agtgecatgt ceggttttea acaaaceatg caaatgetga atgagggeat 4140 cgttcccact gcgatgctgg ttgccaacga tcagatggcg ctgggcgcaa tgcgcgccat 4200 taccgagtcc gggctgcgcg ttggtgcgga tatctcggta gtgggatacg acgataccga 4260 agacagetea tgttatatee egeegttaae eaceateaaa eaggatttte geetgetggg 4320 gcaaaccage gtggaccget tgetgeaact eteteaggge eaggeggtga agggeaatea 4380 getgttgeee gteteaetgg tgaaaagaaa aaceaeeetg gegeecaata egeaaaeege 4440 cteteceege gegttggeeg atteattaat geagetggea egacaggttt eeegactgga 4500

aagcgggcag tgagcgcaac gcaattaatg tg tt cactcattag gcaccccagg 4560 ctttacactt tatgcttccg gctcgtatgt tgtgtgggaartgtgagcgga taacaatttc 4620 acacaggaaa cagctatgac catgattacg gattcactgg ccgtcgtttt acaacgtcgt 4680 gactgggaaa accctggcgt tacccaactt aatcgccttg cagcacatcc ccctttcgcc 4740 agctggcgta atagcgaaga ggcccgcacc gatcgccctt cccaacagtt gcgcagcctg 4800 aatggcgaat ggcgctttgc ctggtttccg gcaccagaag cggtgccgga aagctggctg 4860 gagtgcgatc ttcctgaggc cgatactgtc gtcgtccct caaactggca gatgcacggt 4920 tacgatgcgc ccatctacac caacgtaacc tatcccatta cggtcaatcc gccgtttgtt 4980 cccacggaga atccgacggg ttgttactcg ctcacattta atgttgatga aagctggcta 5040 caggaaggcc agacgcgaat tatttttgat ggcgttggaa tt

<210> 41 <211> 5064 <212> DNA <213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression vector pGEXKT-dp-Pt(TME2)

<400> 41

acgttatcga ctgcacggtg caccaatgct tctggcgtca ggcagccatc ggaagctgtg 60 gtatggctgt gcaggtcgta aatcactgca taattcgtgt cgctcaaggc gcactcccgt 120 tetggataat gttttttgcg eegacateat aaeggttetg geaaatatte tgaaatgage 180 tgttgacaat taatcatcgg ctcgtataat gtgtggaatt gtgagcggat aacaatttca 240 cacaggaaac agtattcatg tcccctatac taggttattg gaaaattaag ggccttgtgc 300 aacccacteg acttettttg gaatatettg aagaaaaata tgaagageat ttgtatgage 360 gcgatgaagg tgataaatgg cgaaacaaaa agtttgaatt gggtttggag tttcccaatc 420 ttccttatta tattgatggt gatgttaaat taacacagtc tatggccatc atacgttata 480 tagctgacaa gcacaacatg ttgggtggtt gtccaaaaga gcgtgcagag atttcaatgc 540 ttgaaggagc ggttttggat attagatacg gtgtttcgag aattgcatat agtaaagact 600 ttgaaactct caaagttgat tttcttagca agctacctga aatgctgaaa atgttcgaag 660 atcgtttatg tcataaaaca tatttaaatg gtgatcatgt aacccatcct gacttcatgt 720 tgtatgacgc tcttgatgtt gttttataca tggacccaat gtgcctggat gcgttcccaa 780 aattagtttg ttttaaaaaa cgtattgaag ctatcccaca aattgataag tacttgaaat 840 ccagcaagta tatagcatgg cctttgcagg gctggcaagc cacgtttggt ggtggcgacc 900 atcctccaaa atcggatctg tctggtggtg gtggtggtct ggttccgcgt ggatccgacc 960 eggaataegt tgttetgetg tteetgetge tggetgaege tegtgtttge tettgeetgt 1020 ggatgatgct gctgatctct caggctgaag cttaggaatt catcgtgact gactgacgat 1080 ctgcctcgcg cgtttcggtg atgacggtga aaacctctga cacatgcagc tcccggagac 1140 ggtcacaget tgtctgtaag eggatgeegg gageagacaa gecegteagg gegegteage 1200 gggtgttggc gggtgtcggg gcgcagccat gacccagtca cgtagcgata gcggagtgta 1260 taattettga agacgaaagg geetegtgat aegeetattt ttataggtta atgteatgat 1320 aataatggtt tettagaegt eaggtggeae ttttegggga aatgtgegeg gaaccectat 1380 ttgtttattt ttctaaatac attcaaatat gtatccgctc atgagacaat aaccctgata 1440 aatgetteaa taatattgaa aaaggaagag tatgagtatt caacatttee gtgtegeeet 1500 tattcccttt tttgcggcat tttgccttcc tgtttttgct cacccagaaa cgctggtgaa 1560 agtaaaagat getgaagate agttgggtge acgagtgggt tacategaae tggateteaa 1620 cageggtaag atcettgaga gttttegeee egaagaaegt ttteeaatga tgageaettt 1680 taaagttetg etatgtggeg eggtattate eegtgttgae geegggeaag ageaactegg 1740 tegeegeata cactattete agaatgaett ggttgagtae teaceagtea eagaaaagea 1800 tettacggat ggcatgacag taagagaatt atgcagtget gccataacca tgagtgataa 1860 cactgeggee aacttactte tgacaacgat eggaggaeeg aaggagetaa eegettttt 1920 gcacaacatg ggggatcatg taactcgcct tgatcgttgg gaaccggagc tgaatgaagc 1980 cataccaaac gacgagcgtg acaccacgat gcctgcagca atggcaacaa cgttgcgcaa 2040 actattaact ggcgaactac ttactctagc ttcccggcaa caattaatag actggatgga 2100 ggcggataaa gttgcaggac cacttctgcg ctcggccctt ccggctggct ggtttattgc 2160 tgataaatct ggagccggtg agcgtgggtc tcgcggtatc attgcagcac tggggccaga 2220 tggtaagccc tcccgtatcg tagttatcta cacgacgggg agtcaggcaa ctatggatga 2280 acgaaataga cagatcgctg agataggtgc ctcactgatt aagcattggt aactgtcaga 2340 ccaagtttac tcatatatac tttagattga tttaaaactt catttttaat ttaaaaggat 2400 ctaggtgaag atcetttttg ataateteat gaccaaaate cettaaegtg agttttegtt 2460

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<210> 42
<211> 5918
<212> DNA
<213> Artificial sequence
<220>
<223> Description of the artificial sequence: expression vector pET32a-dp-Pt(TME1)
```

<400> 42

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<213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression vector pET32a-dp-Pt(TME2)

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<210> 44
<211> 2617
<212> DNA
<213> Artificial sequence
<220>
<223> Description of the artificial sequence: expression vector pT7-7-dp-Pt(TME1)

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aagccatacc aaacgacgag cgtgacacca cg garafigt agcaatggca acaacgttgc 2280 gcaaactatt aactggcgaa ctacttactc tagctte g gcaaacaatta atagactgga 2340 tggaggcgga taaagttgca ggaccacttc tgcgctcggc ccttccggct ggctggttta 2400 ttgctgataa atctggagcc ggtgagcgtg ggtctcgcgg tatcattgca gcactggggc 2460 cagatggtaa gccctcccgt atcgtagtta tctacacgac ggggagtcag gcaactatgg 2520 atgaacgaaa tagacagatc gctgagatag gtgcctcact gattaagcat tggtaactgt 2580 cagaccaagt ttactcatat atactttaga ttgattt

2617

<210> 45 <211> 2599 <212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: expression vector pT7-7-dp-Pt(TME2)

<400> 45

aatteteatg tttgacaget tateategat gataagettg ggetgeaggt egactetaga 60 ggatccccgg gcgcgaattc ctaagettca gcctgagaga tcagcagcat catccacagg 120 caagagcaaa cacgagcgtc agccagcagc aggaacagca gaacaacgta ttccgggtcc 180 atatgtatat ctccttctta aagttaaaca aaattatttc tagagggaaa ccgttgtggt 240 ctccctatag tgagtcgtat taatttcgaa gtctatcaga agttcgaatc gctgggcctc 300 gegegttteg gtgatgaegg tgaaaaecte tgacaeatge ageteeegga gaeggteaca 360 gettgtetgt aageggatge egggageaga caagecegte agggegegte agegggtgtt 420 ggcgggtgtc ggggcgcagc catgacccag tcacgtagcg atagcggagt gtatatactg 480 gcttaactat gcggcatcag agcagattgt actgagagtg caccatagga agatcttccg 540 gaagatette etatgeggtg tgaaataceg cacagatgeg taaggagaaa atacegcate 600 aggegetett cegetteete geteaetgae tegetgeget eggtegtteg getgeggega 660 geggtateag eteaeteaaa ggeggtaata eggttateea eagaateagg ggataaegea 720 ggaaagaaca tgtgagcaaa aggccagcaa aaggccagga accgtaaaaa ggccgcgttg 780 ctggcgtttt tccataggct ccgccccct gacgagcatc acaaaaatcg acgctcaagt 840 cagaggtggc gaaacccgac aggactataa agataccagg cgtttccccc tggaagctcc 900 ctegtgeget etcetgttee gaecetgeeg ettaceggat acetgteege ettteteeet 960 tegggaageg tggegettte teaatgetea egetgtaggt ateteagtte ggtgtaggte 1020 gttcgctcca agctgggctg tgtgcacgaa ccccccgttc agcccgaccg ctgcgcctta 1080 teeggtaact ategtettga gteeaaceeg gtaagacaeg aettategee aetggeagea 1140 gccactggta acaggattag cagagcgagg tatgtaggcg gtgctacaga gttcttgaag 1200 tggtggccta actacggcta cactagaagg acagtatttg gtatctgcgc tctgctgaag 1260 ccagttacct tcggaaaaag agttggtagc tcttgatccg gcaaacaaac caccgctggt 1320 ageggtggtt tttttgtttg caageageag attaegegea gaaaaaaagg ateteaagaa 1380 gateetttga tettttetae ggggtetgae geteagtgga acgaaaaete aegttaaggg 1440 attttggtca tgagattatc aaaaaggatc ttcacctaga tccttttaat tcttgaagac 1500 gaaagggcct cgtgatacgc ctatttttat aggttaatgt catgataata atggtttctt 1560 agacgtcagg tggcactttt cggggaaatg tgcgcggaac ccctatttgt ttattttct 1620 aaatacattc aaatatgtat ccgctcatga gacaataacc ctgataaatg cttcaataat 1680 attgaaaaag gaagagtatg agtattcaac atttccgtgt cgcccttatt cccttttttg 1740 cggcattttg cetteetgtt tttgeteace cagaaacget ggtgaaagta aaagatgetg 1800 aagatcagtt gggtgcacga gtgggttaca tcgaactgga tctcaacagc ggtaagatcc 1860 ttgagagttt tcgccccgaa gaacgttttc caatgatgag cacttttaaa gttctgctat 1920 gtggcgcggt attatcccgt gttgacgccg ggcaagagca actcggtcgc cgcatacact 1980 atteteagaa tgaettggtt gagtaeteae eagteaeaga aaageatett aeggatggea 2040 tgacagtaag agaattatgc agtgctgcca taaccatgag tgataacact gcggccaact 2100 tacttctgac aacgatcgga ggaccgaagg agctaaccgc ttttttgcac aacatggggg 2160 atcatgtaac tegeettgat egttgggaac eggagetgaa tgaagecata ecaaacgaeg 2220 agegtgacae caegatgeet gtageaatgg caacaaegtt gegeaaacta ttaaetggeg 2280 aactacttac tetagettee eggeaacaat taatagactg gatggaggeg gataaagttg 2340 caggaccact tetgegeteg gecetteegg etggetggtt tattgetgat aaatetggag 2400 ccggtgagcg tgggtctcgc ggtatcattg cagcactggg gccagatggt aagccctccc 2460 gtatcgtagt tatctacacg acggggagtc aggcaactat ggatgaacga aatagacaga 2520 tegetgagat aggtgeetea etgattaage attggtaaet gteagaceaa gtttaeteat 2580 2599 atatacttta gattgattt

. "
<210> 46 <211> 271 <212> PRT <213> Artificial sequence
<220> <223> Description of the artificial sequence: fusion protein GST-DP-TME1
<400> 46 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro 1 5 10 15
Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu 20 25 30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu 35 40 45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys 50 55 60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn 65 70 75 80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu 85 90 95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser 100 105 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu 115 120 125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn 130 135 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp 145 150 155 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu 165 170 175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gin Ile Asp Lys Tyr 180 185 190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala 195 200 205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Ser Gly Gly 210 215 220
Gly Gly Gly Leu Val Pro Arg Gly Ser Asp Pro Ile Ala Gly Ala His 225 230 235 240
Trp Gly Val Leu Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp 245 250 255

Ala Lys Val Leu Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala 260 265 270

<211> 265

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: fusion protein GST-DP-TME2

<400> 47

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15

Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu 20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu 35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn 65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu 85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser 100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu 115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn 130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp 145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu 165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr 180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala 195 200 205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Ser Gly Gly 210 215 220

Gly Gly Gly Leu Val Pro Arg Gly Ser Asp Pro Glu Tyr Val Val Leu 225 230 235 240

Leu Phe Leu Leu Leu Ala Asp Ala Arg Val Cys Ser Cys Leu Trp Met 245 250 255

Met Leu Leu Ile Ser Gln Ala Glu Ala 260 265

<210> 48 <211> 170 <212> PRT <213> Artificial sequence
<220> <223> Description of the artificial sequence: fusion protein TrX-DP-TME1
<400> 48 Met Ser Asp Lys Ile Ile His Leu Thr Asp Asp Ser Phe Asp Thr Asp 1 5 10 15
Val Leu Lys Ala Asp Gly Ala Ile Leu Val Asp Phe Trp Ala Glu Trp 20 25 30
Cys Gly Pro Cys Lys Met Ile Ala Pro Ile Leu Asp Glu Ile Ala Asp 35 40 45
Glu Tyr Gln Gly Lys Leu Thr Val Ala Lys Leu Asn Ile Asp Gln Asn 50 55 60
Pro Gly Thr Ala Pro Lys Tyr Gly Ile Arg Gly Ile Pro Thr Leu Leu 65 70 75 80
Leu Phe Lys Asn Gly Glu Val Ala Ala Thr Lys Val Gly Ala Leu Ser 85 90 95
Lys Gly Gln Leu Lys Glu Phe Leu Asp Ala Asn Leu Ala Gly Ser Gly 100 105 110
Ser Gly Ser Pro Lys Ser Asp Leu Ser Gly Gly Gly Gly Leu Val 115 120 125
Pro Arg Gly Ser Asp Pro Ile Ala Gly Ala His Trp Gly Val Leu Ala 130 135 140
Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val Leu Val 145 150 155 160
Val Leu Leu Phe Ala Gly Val Asp Ala 165 170
<210> 49 <211> 161 <212> PRT <213> Artificial sequence
<220> <223> Description of the artificial sequence: fusion protein TrX-DP-TME2
<400> 49 Met Ser Asp Lys Ile Ile His Leu Thr Asp Asp Ser Phe Asp Thr Asp 1 5 10 15
Val Leu Lys Ala Asp Gly Ala Ile Leu Val Asp Phe Trp Ala Glu Trp 20 25 30
Cys Gly Pro Cys Lys Met Ile Ala Pro Ile Leu Asp Glu Ile Ala Asp 35 40 45

<u> </u>
Glu Tyr Gln Gly Lys Leu Thr Val Al. Leu Asn Ile Asp Gln Asn 50 55 60
Pro Gly Thr Ala Pro Lys Tyr Gly Ile Arg Gly Ile Pro Thr Leu Leu 65 70 75 80
Leu Phe Lys Asn Gly Glu Val Ala Ala Thr Lys Val Gly Ala Leu Ser 85 90 95
Lys Gly Gln Leu Lys Glu Phe Leu Asp Ala Asn Leu Ala Gly Ser Gly 100 105 110
Ser Gly Ser Asp Leu Ser Gly Gly Gly Gly Gly Leu Val Pro Arg Gly 115 120 125
Ser Asp Pro Glu Tyr Val Val Leu Leu Phe Leu Leu Leu Ala Asp Ala 130 135 140
Arg Val Cys Ser Cys Leu Trp Met Met Leu Leu Ile Ser Gln Ala Glu 145 150 155 160
Ala
<210> 50 <211> 39 <212> PRT <213> Artificial sequence
<220> <223> Description of the artificial sequence: fusion protein M-DP-TME1
<400> 50 Met Asp Pro Ile Ala Gly Ala His Trp Gly Val Leu Ala Gly Ile Ala 1 5 10 15
Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val Leu Val Val Leu Leu 20 25 30
Leu Phe Ala Gly Val Asp Ala 35
<210> 51 <211> 33 <212> PRT <213> Artificial sequence
<220> <223> Description of the artificial sequence: fusion protein M-DP-TME2
<400> 51 Met Asp Pro Glu Tyr Val Val Leu Leu Phe Leu Leu Leu Ala Asp Ala 1 5 10 15

Arg Val Cys Ser Cys Leu Trp Met Met Leu Leu Ile Ser Gl
n Ala Glu 20 25 30

Ala

<210> 52

<211> 239

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: glutathion transferase (GST)

<400> 52

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro 1 5 10 15

Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu 20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu 35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys 50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn 65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu 85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser 100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu 115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn 130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp 145 150 155 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu 165 170 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr 180 185 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala 195 200 205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Ser Gly Gly 210 215 220

Gly Gly Gly Leu Val Pro Arg Gly Ser Pro Gly Ile His Arg Asp 225 230 235

<210> 53

<211> 170

<212> PRT

<213> Artificial sequence

<220> <223> Description of the artificial sequence thioredoxine (TrX)

<400> 53

Met Ser Asp Lys Ile Ile His Leu Thr Asp Asp Ser Phe Asp Thr Asp 1 5 10 15

Val Leu Lys Ala Asp Gly Ala Ile Leu Val Asp Phe Trp Ala Glu Trp

Cys Gly Pro Cys Lys Met Ile Ala Pro Ile Leu Asp Glu Ile Ala Asp 35 40 45

Glu Tyr Gln Gly Lys Leu Thr Val Ala Lys Leu Asn Ile Asp Gln Asn 50 55 60

Pro Gly Thr Ala Pro Lys Tyr Gly Ile Arg Gly Ile Pro Thr Leu Leu 65 70 75 80

Leu Phe Lys Asn Gly Glu Val Ala Ala Thr Lys Val Gly Ala Leu Ser 85 90 95

Lys Gly Gln Leu Lys Glu Phe Leu Asp Ala Asn Leu Ala Gly Ser Gly
100 105 110

Ser Gly Ser Pro Lys Ser Asp Leu Ser Gly Gly Gly Gly Gly Leu Val 115 120 125

Pro Arg Gly Ser Asp Pro Ile Ala Gly Ala His Trp Gly Val Leu Ala 130 135 140

Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val Leu Val 145 150 155 160

Val Leu Leu Phe Ala Gly Val Asp Ala 165 170